

SEQUENCE LISTING

<110> Haseltine et al.
<120> Human DNA Mismatch Repair Proteins
<130> PF106P3D1
<140> Not assigned
<141> 2002-02-22
<150> PCT/US95/01035
<151> 1995-01-25
<150> 08/468,024
<151> 1995-06-06
<150> 08/465,769
<151> 1995-06-06
<150> 08/294,312
<151> 1994-08-23
<150> 08/210,143
<151> 1994-03-16
<150> 08/187,757
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Gly Val Ile Arg Arg Leu Asp Glu Thr Val Val Asn Arg Ile Ala Ala
10 15 20
ggg gaa gtt atc cag cgg cca gct aat gct atc aaa gag atg att gag 152
Gly Glu Val Ile Gln Arg Pro Ala Asn Ala Ile Lys Glu Met Ile Glu
25 30 35
aac tgt tta gat gca aaa tcc aca agt att caa gtg att gtt aaa gag 200
Asn Cys Leu Asp Ala Lys Ser Thr Ser Ile Gln Val Ile Val Lys Glu
40 45 50
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Lys	Glu	Asp	Leu	Asp	Ile	Val	Cys	Glu	Arg	Phe	Thr	Thr	Ser	Lys	Leu	
70					75					80				85		
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Gln	Ser	Phe	Glu	Asp	Leu	Ala	Ser	Ile	Ser	Thr	Tyr	Gly	Phe	Arg	Gly	
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Glu	Ala	Leu	Ala	Ser	Ile	Ser	His	Val	Ala	His	Val	Thr	Ile	Thr	Thr	
105						110					115					
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120					125					130						
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Lys	Leu	Lys	Ala	Pro	Pro	Lys	Pro	Cys	Ala	Gly	Asn	Gln	Gly	Thr	Gln	
135					140					145						
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Ile	Thr	Val	Glu	Asp	Leu	Phe	Tyr	Asn	Ile	Ala	Thr	Arg	Arg	Lys	Ala	
150					155					160			165			
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Leu	Lys	Asn	Pro	Ser	Glu	Glu	Tyr	Gly	Lys	Ile	Leu	Glu	Val	Val	Gly	
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Arg	Tyr	Ser	Val	His	Asn	Ala	Gly	Ile	Ser	Phe	Ser	Val	Lys	Lys	Gln	
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Gly	Glu	Thr	Val	Ala	Asp	Val	Arg	Thr	Leu	Pro	Asn	Ala	Ser	Thr	Val	
200					205					210						
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Asp	Asn	Ile	Arg	Ser	Val	Phe	Gly	Asn	Ala	Val	Ser	Arg	Glu	Leu	Ile	
215					220					225						
gaa	att	gga	tgt	gag	gat	aaa	acc	cta	gcc	ttc	aaa	atg	aat	ggt	tac	776
Glu	Ile	Gly	Cys	Glu	Asp	Lys	Thr	Leu	Ala	Phe	Lys	Met	Asn	Gly	Tyr	
230					235					240			245			
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Ile	Ser	Asn	Ala	Asn	Tyr	Ser	Val	Lys	Lys	Cys	Ile	Phe	Leu	Leu	Phe	
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265					270					275						
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Thr	Val	Tyr	Ala	Ala	Tyr	Leu	Pro	Lys	Asn	Thr	His	Pro	Phe	Leu	Tyr	
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Leu Ser Leu Glu Ile Ser Pro Gln Asn Val Asp Val Asn Val His Pro			
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Thr Lys His Glu Val His Phe Leu His Glu Glu Ser Ile Leu Glu Arg			
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gtg cag cag cac atc gag agc aag ctc ctg ggc tcc aat tcc tcc agg			1064
Val Gln Gln His Ile Glu Ser Lys Leu Leu Gly Ser Asn Ser Ser Arg			
330	335	340	
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Met Tyr Phe Thr Gln Thr Leu Leu Pro Gly Leu Ala Gly Pro Ser Gly			
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Glu Met Val Lys Ser Thr Ser Leu Thr Ser Ser Ser Thr Ser Gly			
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Ser Ser Asp Lys Val Tyr Ala His Gln Met Val Arg Thr Asp Ser Arg			
375	380	385	
gaa cag aag ctt gat gca ttt ctg cag cct ctg agc aaa ccc ctg tcc			1256
Glu Gln Lys Leu Asp Ala Phe Leu Gln Pro Leu Ser Lys Pro Leu Ser			
390	395	400	405
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Ser Gln Pro Gln Ala Ile Val Thr Glu Asp Lys Thr Asp Ile Ser Ser			
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Gly Arg Ala Arg Gln Gln Asp Glu Glu Met Leu Glu Leu Pro Ala Pro			
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Gly Thr Ser Glu Met Ser Glu Lys Arg Gly Pro Thr Ser Ser Asn Pro			
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470	475	480	485
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Ser Arg Lys Glu Met Thr Ala Ala Cys Thr Pro Arg Arg Arg Ile Ile			
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Asn Leu Thr Ser Val Leu Ser Leu Gln Glu Glu Ile Asn Glu Gln Gly			
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His Glu Val Leu Arg Glu Met Leu His Asn His Ser Phe Val Gly Cys			
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Thr Glu Val Asn Trp Asp Glu Glu Lys Glu Cys Phe Glu Ser Leu Ser			
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Asn Ser Trp Lys Trp Thr Val Glu His Ile Val Tyr Lys Ala Leu Arg			
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Gln Leu Ala Asn Leu Pro Asp Leu Tyr Lys Val Phe Glu Arg Cys			
745	750	755	
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ttgtatcaaa gtgtatata caaagtgtac caacataagt gttggtagca cttaagactt			2432
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35 40 45

Val Ile Val Lys Glu Gly Leu Lys Leu Ile Gln Ile Gln Asp Asn
50 55 60

Gly Thr Gly Ile Arg Lys Glu Asp Leu Asp Ile Val Cys Glu Arg Phe
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Thr Thr Ser Lys Leu Gln Ser Phe Glu Asp Leu Ala Ser Ile Ser Thr
85 90 95

Tyr Gly Phe Arg Gly Glu Ala Leu Ala Ser Ile Ser His Val Ala His
100 105 110

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115 120 125

Ser Tyr Ser Asp Gly Lys Leu Lys Ala Pro Pro Lys Pro Cys Ala Gly
130 135 140

Asn Gln Gly Thr Gln Ile Thr Val Glu Asp Leu Phe Tyr Asn Ile Ala
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Thr Arg Arg Lys Ala Leu Lys Asn Pro Ser Glu Glu Tyr Gly Lys Ile
165 170 175

Leu Glu Val Val Gly Arg Tyr Ser Val His Asn Ala Gly Ile Ser Phe
180 185 190

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225 230 235 240

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290 295 300

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325 330 335

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580 585 590

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625 630 635 640

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660 665 670

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675 680 685

Gln Tyr Ile Ser Glu Glu Ser Thr Leu Ser Gly Gln Gln Ser Glu Val
690 695 700

Pro Gly Ser Ile Pro Asn Ser Trp Lys Trp Thr Val Glu His Ile Val
705 710 715 720

Tyr Lys Ala Leu Arg Ser His Ile Leu Pro Pro Lys His Phe Thr Glu
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Leu Ser Ser Gln Ile Ile Thr Ser Val Val Ser Val Val Lys Glu
15 20 25

ctt att gaa aac tcc ttg gat gct ggt gcc aca agc gta gat gtt aaa 209
Leu Ile Glu Asn Ser Leu Asp Ala Gly Ala Thr Ser Val Asp Val Lys
30 35 40

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Leu Glu Asn Tyr Gly Phe Asp Lys Ile Glu Val Arg Asp Asn Gly Glu
45 50 55

ggc atc aag gct gtt gat gca cct gta atg gca atg aag tac tac acc 305
Gly Ile Lys Ala Val Asp Ala Pro Val Met Ala Met Lys Tyr Tyr Thr
60 65 70 75

tca aaa ata aat agt cat gaa gat ctt gaa aat ttg aca act tac ggt 353
Ser Lys Ile Asn Ser His Glu Asp Leu Glu Asn Leu Thr Thr Tyr Gly
80 85 90

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401			
Phe Arg Gly Glu Ala Leu Gly Ser Ile Cys Cys Ile Ala Glu Val Leu			
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Ile Thr Thr Arg Thr Ala Ala Asp Asn Phe Ser Thr Gln Tyr Val Leu			
110	115	120	
gat ggc agt ggc cac ata ctt tct cag aaa cct tca cat ctt ggt caa			497
Asp Gly Ser Gly His Ile Leu Ser Gln Lys Pro Ser His Leu Gly Gln			
125	130	135	
ggt aca act gta act gct tta aga tta ttt aag aat cta cct gta aga			545
Gly Thr Thr Val Thr Ala Leu Arg Leu Phe Lys Asn Leu Pro Val Arg			
140	145	150	155
aag cag ttt tac tca act gca aaa aaa tgt aaa gat gaa ata aaa aag			593
Lys Gln Phe Tyr Ser Thr Ala Lys Lys Cys Lys Asp Glu Ile Lys Lys			
160	165	170	
atc caa gat ctc ctc atg agc ttt ggt atc ctt aaa cct gac tta agg			641
Ile Gln Asp Leu Leu Met Ser Phe Gly Ile Leu Lys Pro Asp Leu Arg			
175	180	185	
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Ile Val Phe Val His Asn Lys Ala Val Ile Trp Gln Lys Ser Arg Val			
190	195	200	
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Ser Asp His Lys Met Ala Leu Met Ser Val Leu Gly Thr Ala Val Met			
205	210	215	
aac aat atg gaa tcc ttt cag tac cac tct gaa gaa tct cag att tat			785
Asn Asn Met Glu Ser Phe Gln Tyr His Ser Glu Glu Ser Gln Ile Tyr			
220	225	230	235
ctc agt gga ttt ctt cca aag tgt gat gca gac cac tct ttc act agt			833
Leu Ser Gly Phe Leu Pro Lys Cys Asp Ala Asp His Ser Phe Thr Ser			
240	245	250	
ctt tca aca cca gaa aga agt ttc atc ttc ata aac agt cga cca gta			881
Leu Ser Thr Pro Glu Arg Ser Phe Ile Phe Ile Asn Ser Arg Pro Val			
255	260	265	
cat caa aaa gat atc tta aag tta atc cga cat cat tac aat ctg aaa			929
His Gln Lys Asp Ile Leu Lys Leu Ile Arg His His Tyr Asn Leu Lys			
270	275	280	
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Cys Leu Lys Glu Ser Thr Arg Leu Tyr Pro Val Phe Phe Leu Lys Ile			
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Asp Val Pro Thr Ala Asp Val Asp Val Asn Leu Thr Pro Asp Lys Ser			
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caa gta tta tta caa aat aag gaa tct gtt tta att gct ctt gaa aat			1073
Gln Val Leu Leu Gln Asn Lys Glu Ser Val Leu Ile Ala Leu Glu Asn			
320	325	330	

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1121			
Leu Met Thr Thr Cys Tyr Gly Pro Leu Pro Ser Thr Asn Ser Tyr Glu			
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aat aat aaa aca gat gtt tcc gca gct gac atc gtt ctt agt aaa aca			1169
Asn Asn Lys Thr Asp Val Ser Ala Ala Asp Ile Val Leu Ser Lys Thr			
350	355	360	
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Ala Glu Thr Asp Val Leu Phe Asn Lys Val Glu Ser Ser Gly Lys Asn			
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380	385	390	395
aat gat gaa tct gga aaa aac act gat gat tgt tta aat cac cag ata			1313
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Ile Asp Lys Asn Thr Lys Asn Ala Phe Gln Asp Ile Ser Met Ser Asn			
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480	485	490	
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Glu Ile Ser Ala Asp Glu Trp Ser Arg Gly Asn Ile Leu Lys Asn Ser			
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Val Gly Glu Asn Ile Glu Pro Val Lys Ile Leu Val Pro Glu Lys Ser			
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Leu Pro Cys Lys Val Ser Asn Asn Tyr Pro Ile Pro Glu Gln Met			
525	530	535	
aat ctt aat gaa gat tca tgt aac aaa aaa tca aat gta ata gat aat			1745
Asn Leu Asn Glu Asp Ser Cys Asn Lys Ser Asn Val Ile Asp Asn			
540	545	550	555
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caa att gaa gaa ctg tgg aag aca ttg agt gaa gag gaa aaa ctg aaa Gln Ile Glu Glu Leu Trp Lys Thr Leu Ser Glu Glu Lys Leu Lys 605	610	615		1937
tat gaa gag aag gct act aaa gac ttg gaa cga tac aat agt caa atg Tyr Glu Glu Lys Ala Thr Lys Asp Leu Glu Arg Tyr Asn Ser Gln Met 620	625	630	635	1985
aag aga gcc att gaa cag gag tca caa atg tca cta aaa gat ggc aga Lys Arg Ala Ile Glu Gln Glu Ser Gln Met Ser Leu Lys Asp Gly Arg 640	645	650		2033
aaa aag ata aaa ccc acc agc gca tgg aat ttg gcc cag aag cac aag Lys Lys Ile Lys Pro Thr Ser Ala Trp Asn Leu Ala Gln Lys His Lys 655	660	665		2081
tta aaa acc tca tta tct aat caa cca aaa ctt gat gaa ctc ctt cag Leu Lys Thr Ser Leu Ser Asn Gln Pro Lys Leu Asp Glu Leu Leu Gln 670	675	680		2129
tcc caa att gaa aaa aga agg agt caa aat att aaa atg gta cag atc Ser Gln Ile Glu Lys Arg Arg Ser Gln Asn Ile Lys Met Val Gln Ile 685	690	695		2177
ccc ttt tct atg aaa aac tta aaa ata aat ttt aag aaa caa aac aaa Pro Phe Ser Met Lys Asn Leu Lys Ile Asn Phe Lys Lys Gln Asn Lys 700	705	710	715	2225
gtt gac tta gaa gag aag gat gaa cct tgc ttg atc cac aat ctc agg Val Asp Leu Glu Glu Lys Asp Glu Pro Cys Leu Ile His Asn Leu Arg 720	725	730		2273
ttt cct gat gca tgg cta atg aca tcc aaa aca gag gta atg tta tta Phe Pro Asp Ala Trp Leu Met Thr Ser Lys Thr Glu Val Met Leu Leu 735	740	745		2321
aat cca tat aga gta gaa gaa gcc ctg cta ttt aaa aga ctt ctt gag Asn Pro Tyr Arg Val Glu Glu Ala Leu Leu Phe Lys Arg Leu Leu Glu 750	755	760		2369
aat cat aaa ctt cct gca gag cca ctg gaa aag cca att atg tta aca Asn His Lys Leu Pro Ala Glu Pro Leu Glu Lys Pro Ile Met Leu Thr 765	770	775		2417
gag agt ctt ttt aat gga tct cat tat tta gac gtt tta tat aaa atg Glu Ser Leu Phe Asn Gly Ser His Tyr Leu Asp Val Leu Tyr Lys Met 780	785	790	795	2465
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800	805	810	
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Arg Leu Thr Ala Asn Gly Phe Lys Ile Lys Leu Ile Pro Gly Val Ser			
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Ile Thr Glu Asn Tyr Leu Glu Ile Glu Gly Met Ala Asn Cys Leu Pro			
830	835	840	
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Phe Tyr Gly Val Ala Asp Leu Lys Glu Ile Leu Asn Ala Ile Leu Asn			
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aga aat gca aag gaa gtt tat gaa tgt aga cct cgc aaa gtg ata agt			2705
Arg Asn Ala Lys Glu Val Tyr Glu Cys Arg Pro Arg Lys Val Ile Ser			
860	865	870	875
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His Leu Thr Tyr Leu Pro Glu Thr Thr			
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Leu Gly Ser Ile Cys Cys Ile Ala Glu Val Leu Ile Thr Thr Arg Thr
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Ala Ala Asp Asn Phe Ser Thr Gln Tyr Val Leu Asp Gly Ser Gly His
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Ile Leu Ser Gln Lys Pro Ser His Leu Gly Gln Gly Thr Thr Val Thr
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Ala Leu Arg Leu Phe Lys Asn Leu Pro Val Arg Lys Gln Phe Tyr Ser
145 150 155 160

Thr Ala Lys Lys Cys Lys Asp Glu Ile Lys Lys Ile Gln Asp Leu Leu
165 170 175

Met Ser Phe Gly Ile Leu Lys Pro Asp Leu Arg Ile Val Phe Val His
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Asn Lys Ala Val Ile Trp Gln Lys Ser Arg Val Ser Asp His Lys Met
195 200 205

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Phe Gln Tyr His Ser Glu Glu Ser Gln Ile Tyr Leu Ser Gly Phe Leu
225 230 235 240

Pro Lys Cys Asp Ala Asp His Ser Phe Thr Ser Leu Ser Thr Pro Glu
245 250 255

Arg Ser Phe Ile Phe Ile Asn Ser Arg Pro Val His Gln Lys Asp Ile
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Thr Arg Leu Tyr Pro Val Phe Phe Leu Lys Ile Asp Val Pro Thr Ala
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325 330 335

Tyr Gly Pro Leu Pro Ser Thr Asn Ser Tyr Glu Asn Asn Lys Thr Asp
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Val Ser Ala Ala Asp Ile Val Leu Ser Lys Thr Ala Glu Thr Asp Val
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Thr Ser Val Ile Pro Phe Gln Asn Asp Met His Asn Asp Glu Ser Gly
385 390 395 400

Lys Asn Thr Asp Asp Cys Leu Asn His Gln Ile Ser Ile Gly Asp Phe
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Gly Tyr Gly His Cys Ser Ser Glu Ile Ser Asn Ile Asp Lys Asn Thr
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Asn Glu Glu Glu Ala Gly Leu Glu Asn Ser Ser Glu Ile Ser Ala Asp
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Ser Cys Asn Lys Lys Ser Asn Val Ile Asp Asn Lys Ser Gly Lys Val
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565 570 575

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580 585 590

Asn Pro Lys Thr Ser Leu Glu Asp Ala Thr Leu Gln Ile Glu Glu Leu
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Trp Lys Thr Leu Ser Glu Glu Lys Leu Lys Tyr Glu Glu Lys Ala
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Thr Lys Asp Leu Glu Arg Tyr Asn Ser Gln Met Lys Arg Ala Ile Glu
625 630 635 640

Gln Glu Ser Gln Met Ser Leu Lys Asp Gly Arg Lys Lys Ile Lys Pro
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Ser Asn Gln Pro Lys Leu Asp Glu Leu Leu Gln Ser Gln Ile Glu Lys
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Arg Arg Ser Gln Asn Ile Lys Met Val Gln Ile Pro Phe Ser Met Lys
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Asn Leu Lys Ile Asn Phe Lys Lys Gln Asn Lys Val Asp Leu Glu Glu
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Lys Asp Glu Pro Cys Leu Ile His Asn Leu Arg Phe Pro Asp Ala Trp
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Glu Glu Ala Leu Leu Phe Lys Arg Leu Leu Glu Asn His Lys Leu Pro
755 760 765

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770 775 780

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Gly Phe Lys Ile Lys Leu Ile Pro Gly Val Ser Ile Thr Glu Asn Tyr
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Val Tyr Glu Cys Arg Pro Arg Lys Val Ile Ser Tyr Leu Glu Gly Glu
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ggg gta gaa gaa gaa aac ttc gaa ggc tta act ctg aaa cat cac aca Gly Val Glu Glu Glu Asn Phe Glu Gly Leu Thr Leu Lys His His Thr 75 80 85				291
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aaa gcg cct gaa act gac gac tct ttt tca gat gtg gac tgc cat tca Lys Ala Pro Glu Thr Asp Asp Ser Phe Ser Asp Val Asp Cys His Ser 540	545	550		1683
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gca aag att tgt cct gga gaa aat caa gca gcc gaa gat gaa cta aga Ala Lys Ile Cys Pro Gly Glu Asn Gln Ala Ala Glu Asp Glu Leu Arg 650	655	660	665	2019
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Gly Lys Arg Gln Pro Val Val Cys Thr Gly Gly Ser Pro Ser Ile Lys
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Ile Ser Gln Cys Thr His Gly Val Gly Arg Ser Ser Thr Asp Arg Gln
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Ser Leu Pro Thr Ser Lys Asn Trp Thr Phe Gly Pro Gln Asp Val Asp
770 775 780

Glu Leu Ile Phe Met Leu Ser Asp Ser Pro Gly Val Met Cys Arg Pro
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Ser Arg Val Lys Gln Met Phe Ala Ser Arg Ala Cys Arg Lys Ser Val
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Met Ile Gly Thr Ala Leu Asn Thr Ser Glu Met Lys Lys Leu Ile Thr
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His Met Gly Glu Met Asp His Pro Trp Asn Cys Pro His Gly Arg Pro
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<400> 8
tcgtggcagg ggttattcg

19

<210> 9
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> hMLH1 sense primer

<400> 9
ctacccaatg cctcaaccg

19

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<223> hMLH1 sense primer	
<400> 10	22
gagaactgat agaaaattgga tg	
<210> 11	
<211> 18	
<212> DNA	
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<223> hMLH1 sense primer	
<400> 11	18
gggacatgag gttctccg	
<210> 12	
<211> 19	
<212> DNA	
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<223> hMLH1 sense primer	
<400> 12	19
gggctgtgtg aatcctcag	
<210> 13	
<211> 20	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> hMLH1 antisense primer	
<400> 13	20
cggttcacca ctgtctcg	
<210> 14	
<211> 18	
<212> DNA	
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<223> hMLH1 antisense primer	
<400> 14	18
tccaggatgc tctcctcg	

<210> 15
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> hMLH1 antisense primer

<400> 15
caagtcctgg tagcaaagt c 20

<210> 16
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> hMLH1 antisense primer

<400> 16
atggcaaggt caaagagcg 19

<210> 17
<211> 22
<212> DNA
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<220>
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<220>
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<400> 17
caacaatgtt ttcagnaaat cc 22

<210> 18
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> hMLH1 antisense primer

<400> 18
ttgatataaac actttgtatc g 21

<210> 19
<211> 21
<212> DNA
<213> Artificial Sequence

<220>

<223> hMLH1 antisense primer

<400> 19
ggaatactat cagaaggcaa g

21

<210> 20
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<212> DNA
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<220>
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<400> 20
acagagcaag ttactcagat g

21

<210> 21
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<220>
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<400> 21
gtacacaatg caggcattag

20

<210> 22
<211> 21
<212> DNA
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<220>
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<400> 22
aatgtggatg ttaatgtgca c

21

<210> 23
<211> 18
<212> DNA
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<220>
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<400> 23
ctgacacctcgat cttcctac

18

<210> 24
<211> 19
<212> DNA
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<220>

<223> hMLH1 sense primer

<400> 24
cagcaagatg aggagatgc 19

<210> 25
<211> 21
<212> DNA
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<220>
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<400> 25
ggaaaatggtg gaagatgatt c 21

<210> 26
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<212> DNA
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<220>
<223> hMLH1 sense primer

<400> 26
cttctcaaca ccaagc 16

<210> 27
<211> 21
<212> DNA
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<220>
<223> hMLH1 sense primer

<400> 27
gaaattgatg aggaagggaa c 21

<210> 28
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> hMLH1 sense primer

<400> 28
cttctgattg acaactatgt gc 22

<210> 29
<211> 22
<212> DNA
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<220>

<223> hMLH1 sense primer

<400> 29
cacagaagat ggaaatatcc tg 22

<210> 30
<211> 20
<212> DNA
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<400> 30
gtgttggtag cacttaagac 20

<210> 31
<211> 20
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<220>
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<400> 31
tttcccatat tcttcacttg 20

<210> 32
<211> 19
<212> DNA
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<220>
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<400> 32
gtaacatgag ccacatggc 19

<210> 33
<211> 19
<212> DNA
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<220>
<223> hMLH1 antisense primer

<400> 33
ccactgtctc gtccagccg 19

<210> 34
<211> 26
<212> DNA
<213> Artificial Sequence

<220>

<223> hMLH1 5' primer with BamHI restriction site

<400> 34

cgggatccat gtcgttcgtg gcaggg

26

<210> 35

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> hMLH1 3' primer with XbaI restriction site

<400> 35

gctctagatt aacacctctc aaagac

26

<210> 36

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> hMLH1 primer useful for amplifying codons 1 to 394

<400> 36

gcatctagac gtttccttgg c

21

<210> 37

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> primer useful for amplifying codons 1 to 394 of hMLH1

<400> 37

catccaagct tctgttcccg

20

<210> 38

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> primer useful for amplifying codons 326 to 729 of hMLH1

<400> 38

ggggtgtcagc agcacatcg

19

<210> 39

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> primer useful for amplifying codons 326 to 729 of hMLH1

<400> 39

ggaggcagaa tgtgtgagcg

20

<210> 40

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> primer useful for amplifying codons 602 to 756 plus 128 nucleotides of 3' untranslated sequence of hMLH1

<400> 40

tcccaaagaa ggacttgct

19

<210> 41

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> primer useful for amplifying codons 602 to 756 plus 128 nucleotides of 3' untranslated sequence of hMLH1

<400> 41

agtataagtc ttaagtgcta cc

22

<210> 42

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> primer useful for amplifying codons 578 to 632 of hMLH1

<400> 42

ttttaggttt ctcacctgcc

20

<210> 43

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> primer useful for amplifying codons 578 to 632 of hMLH1

<400> 43

gttatctgcc cacctcagc

19

<210> 44

<211> 59

<212> DNA

<213> Artificial Sequence

<220>
<223> primer useful for amplifying codons 1 to 394 of hMLH1 wherein PCR product may be used for coupled transcription-translation

<400> 44
ggatcctaat acgactcact atagggagac caccatggca tctagacgtt tcccttggc 59

<210> 45
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> primer useful for amplifying codons 1 to 394 of hMLH1 wherein PCR product may be used for coupled transcription-translation

<400> 45
catccaagct tctgttcccg 20

<210> 46
<211> 56
<212> DNA
<213> Artificial Sequence

<220>
<223> primer useful for amplifying codons 326 to 729 of hMLH1 wherein PCR product may be used for coupled transcription-translation

<400> 46
ggatcctaat acgactcact atagggagac caccatgggg gtgcagcagc acatcg 56

<210> 47
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> primer useful for amplifying codons 326 to 729 of hMLH1 wherein PCR product may be used for coupled transcription-translation

<400> 47
ggaggcagaa tgtgtgagcg 20

<210> 48
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> hMLH2 5' primer with a BamHI restriction site

<400> 48
cgggatccat gaaacaattt cctgcggc 28

<210> 49
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> hMLH2 3' primer with XbaI restriction site

<400> 49
gctctagacc agactcatgc tgtttt 26

<210> 50
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> hMLH3 5' primer with a BamHI restriction site

<400> 50
cgggatccat ggagcgagct gagagc 26

<210> 51
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> hMLH3 3' primer with XbaI restriction site

<400> 51
gctctagagt gaagactctg tct 23

<210> 52
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> hMLH2 primer

<400> 52
aagctgctct gttaaaagcg 20

<210> 53
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> hMLH2 primer

<400> 53
gcaccagcat ccaaggag 18

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<210> 54
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> hMLH3 primer

<400> 54
caaccatgag acacatcgc 19

<210> 55
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> hMLH3 primer

<400> 55
aggttagtga agactctgtc 20

<210> 56
<211> 53
<212> DNA
<213> Artificial Sequence

<220>
<223> primer useful for amplifying codons 1 to 500 of hMLH2

<400> 56
ggatcctaat acgactcact atagggagac caccatggaa caattgcctg cgg 53

<210> 57
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> primer useful for amplifying codons 1 to 500 of hMLH2

<400> 57
cctgctccac tcatctgc 18

<210> 58
<211> 60
<212> DNA
<213> Artificial Sequence

<220>
<223> primer useful for amplifying codons 270 to 755 of hMLH2

<400> 58
ggatcctaat acgactcact atagggagac caccatggaa gatatcttaa agttaatccg 60

<210> 59
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> primer useful for amplifying codons 270 to 755 of hMLH2

<400> 59
ggcttcttct actctataatg g 21

<210> 60
<211> 58
<212> DNA
<213> Artificial Sequence

<220>
<223> primer useful for amplifying from codon 485 to the translation termination site at codon 933 of hMLH2

<400> 60
ggatcctaat acgactcaact ataggagac caccatggca ggtcttgaaa actcttcg 58

<210> 61
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> primer useful for amplifying from codon 485 to the translation termination site at codon 933 of hMLH2

<400> 61
aaaacaagtc agtgaatcct c 21

<210> 62
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> 3' primer useful for amplifying up to codon 369 of hMLH2

<400> 62
aagcacatct gtttctgctg 20

<210> 63
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> 3' primer useful for amplifying up to codon 290 of hMLH2

<400> 63
acgagtagat tccttttaggc 20

<210> 64
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> 3' primer useful for amplifying up to codon 214 of hMLH2

<400> 64
cagaactgac atgagagcc

19

<210> 65
<211> 52
<212> DNA
<213> Artificial Sequence

<220>
<223> primer useful for amplifying codons 1 to 863 hMLH3

<400> 65
ggatcctaat acgactcact atagggagac caccatggag cgagctgaga gc

52

<210> 66
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> primer useful for amplifying codons 1 to 863 hMLH3

<400> 66
aggtagtgtga agactctgtc

20

<210> 67
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> primer useful for amplifying up to codon 472 of hMLH3

<400> 67
ctgaggtctc agcaggc

17

<210> 68
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> primer useful for amplifying codons 415 to 863 of hMLH3

<400> 68
ggatcctaat acgactcact atagggagac caccatggtg tccatttcca gactgcg

57

<210> 69
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> primer useful for amplifying codons 415 to 863 of hMLH3

<400> 69
aggtagtga agactctgtc

20

<210> 70
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> primer useful for amplifying codons 195 to 233 of hMLH2

<400> 70
ttatttggca gaaaagcaga g

21

<210> 71
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> primer useful for amplifying codons 195 to 233 of hMLH2

<400> 71
ttaaaaagact aacctcttgc c

21

<210> 72
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> sequencing primer useful for sequencing codons 195 to 233 of hMLH2

<400> 72
ctgctgttat gaacaatatg g

21

<210> 73
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> primer useful for amplifying codons 233 to 257 of hMLH3

<400> 73

cagaaggagt tgcaaagcc
19

<210> 74
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> primer useful for amplifying codons 233 to 257 of hMLH3

<400> 74
aaaccgtact cttcacacac

20

<210> 75
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> primer useful for amplifying codons 347 of 377 of hMLH3

<400> 75
gaggaaaagc ttttgttggc

20

<210> 76
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> primer useful for amplifying codons 347 of 377 of hMLH3

<400> 76
cagtggctgc tgactgac

18

<210> 77
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> primer useful for amplifying codons 439 to 472 of hMLH3

<400> 77
tccagaacca agaaggagc

19

<210> 78
<211> 16
<212> DNA
<213> Artificial Sequence

<220>
<223> primer useful for amplifying codons 439 to 472 of hMLH3

<400> 78
tgaggtctca gcaggc

16